



# results of BLAST

BLASTP 2.2.14 [May-07-2006]

## Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1150326844-7029-23201072992.BLASTQ4

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
3,695,564 sequences; 1,269,795,892 total letters

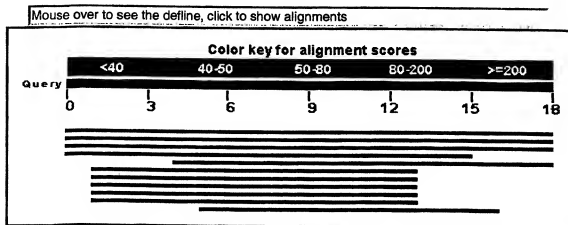
If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

**Query=**

Length=18

## Distribution of 11 Blast Hits on the Query Sequence



[Tree view](#) NEW

Sequences producing significant alignments:

Score  
(Bits) E  
Value

<a href="#">gi 54696716 gb AAV38730.1 </a>	tumor necrosis factor receptor sup...	<a href="#">56.2</a>	1e-07	
<a href="#">gi 339758 gb AAA36755.1 </a>	tumor necrosis factor receptor	<a href="#">56.2</a>	1e-07	
<a href="#">gi 37359212 gb AAN72434.1 </a>	soluble tumor necrosis factor rece...	<a href="#">56.2</a>	1e-07	
<a href="#">gi 825701 emb CAA56324.1 </a>	p75 TNF receptor [Homo sapiens]	<a href="#">46.4</a>	1e-04	
<a href="#">gi 6683130 dbj BAA89052.1 </a>	tumor necrosis factor receptor 2 [Hom	<a href="#">43.9</a>	8e-04	
<a href="#">gi 15030259 gb AAH11399.1 </a>	SYK protein [Homo sapiens] >gi 559...	<a href="#">28.6</a>	30	
<a href="#">gi 515871 emb CAAS1970.1 </a>	protein tyrosin kinase [Homo sapiens]	<a href="#">28.6</a>	30	

EXHIBIT D

<a href="#">gi 12804475 gb AAH01645.1</a>	Spleen tyrosine kinase [Homo sapie...	28.6	30	
<a href="#">gi 448916 prf 1918215A</a>	protein Tyr kinase	28.6	30	
<a href="#">gi 1092813 prf 2101280A</a>	p72syk protein	28.6	30	
<a href="#">gi 89061682 ref XP_944591.1</a>	PREDICTED: similar to dynein, ax...	26.1	174	

# Alignments

> ☐ [gi|54696716|gb|AAV38730.1](#) tumor necrosis factor receptor superfamily, member  
[gi|31419790|gb|AAH52977.1](#) Tumor necrosis factor receptor 2, precursor [Homo sap  
[gi|32891819|gb|AAP88939.1](#) tumor necrosis factor receptor superfamily, member 1B  
[gi|55663791|emb|CAH73721.1](#) tumor necrosis factor receptor superfamily, member 1  
[gi|56202703|emb|CAI19225.1](#) tumor necrosis factor receptor superfamily, member 1  
[gi|4507577|ref|NP\\_001057.1](#) tumor necrosis factor receptor 2 precursor [Homo sap  
[gi|29725900|gb|AAO89076.1](#) tumor necrosis factor receptor superfamily, member 1B  
[gi|61356471|gb|AAK41249.1](#) tumor necrosis factor receptor superfamily member 1B [s  
construct]  
[gi|21264534|sp|P20333|TNFR1B\\_HUMAN](#) Tumor necrosis factor receptor superfamily mem  
(Tumor necrosis factor receptor 2) (TNF-R2) (Tumor necrosis  
factor receptor type II) (p75) (p80 TNF-alpha receptor) (CD120b  
antigen) (Etanercept) [Contains: Tumor necrosis factor  
receptor superfamily member 1b, membrane form; Tumor necrosis  
factor-binding protein 2 (TBP2) (TBP-2)]  
[gi|1469541|gb|AAC50622.1](#) tumor necrosis factor receptor  
[gi|189186|gb|AAA59929.1](#) tumor necrosis factor receptor  
Length=461

Score = 56.2 bits (125), Expect = 1e-07  
Identities = 17/18 (94%), Positives = 17/18 (94%), Gaps = 0/18 (0%)

Query 1 LPAQVAFBPPYAEPEGSTC 18  
LPAQVAF PYAEPEGSTC  
Sbjct 23 LPAQVAFTPYAEPEGSTC 40

> ☐ [gi|339758|gb|AAA36755.1](#) tumor necrosis factor receptor  
Length=461

Score = 56.2 bits (125), Expect = 1e-07  
Identities = 17/18 (94%), Positives = 17/18 (94%), Gaps = 0/18 (0%)

Query 1 LPAQVAFBPPYAEPEGSTC 18  
LPAQVAF PYAEPEGSTC  
Sbjct 23 LPAQVAFTPYAEPEGSTC 40

> ☐ [gi|37359212|gb|AAN72434.1](#) soluble tumor necrosis factor receptor superfamily  
[Homo sapiens]  
Length=268

Score = 56.2 bits (125), Expect = 1e-07  
Identities = 17/18 (94%), Positives = 17/18 (94%), Gaps = 0/18 (0%)

Query 1 LPAQVAFBPPYAEPEGSTC 18  
LPAQVAF PYAEPEGSTC

Sbjct 23 LPAQVAFBYPYAPEPGSTC 40

> [gi|825701|emb|CAA56324.1](#) [p75 TNF receptor \[Homo sapiens\]](#)  
Length=37

Score = 46.4 bits (102), Expect = 1e-04  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 LPAQVAFBYPYAPEPG 15  
LPAQVAF PYAPEPG  
Sbjct 23 LPAQVAFBYPYAPEPG 37

> [gi|6683130|dbj|BAA89052.1](#) [tumor necrosis factor receptor 2 \[Homo sapiens\]](#)  
Length=33

Score = 43.9 bits (96), Expect = 8e-04  
Identities = 13/14 (92%), Positives = 13/14 (92%), Gaps = 0/14 (0%)

Query 5 VAFBYPYAPEPGSTC 18  
VAF PYAPEPGSTC  
Sbjct 1 VAFBYPYAPEPGSTC 14

> [gi|15030259|gb|AAH11399.1](#) [SYK protein \[Homo sapiens\]](#)  
[gi|55958427|emb|CAI16875.1](#) [spleen tyrosine kinase \[Homo sapiens\]](#)  
[gi|496900|emb|CAA82737.1](#) [protein-tyrosine kinase \[Homo sapiens\]](#)  
Length=612

Score = 28.6 bits (60), Expect = 30  
Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBYPYAPE 13  
PAQ V+F+PY PE  
Sbjct 285 PAQGNRQESTVSPNPEPE 303

> [gi|515871|emb|CAA51970.1](#) [protein tyrosin kinase \[Homo sapiens\]](#)  
Length=630

Score = 28.6 bits (60), Expect = 30  
Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBYPYAPE 13  
PAQ V+F+PY PE  
Sbjct 303 PAQGNRQESTVSPNPEPE 321

> [gi|12804475|gb|AAH01645.1](#) [Spleen tyrosine kinase \[Homo sapiens\]](#)  
[gi|55958428|emb|CAI16876.1](#) [spleen tyrosine kinase \[Homo sapiens\]](#)  
[gi|1174527|sp|P43405|KSYK\\_HUMAN](#) [Tyrosine-protein kinase SYK \(Spleen tyrosine kin](#)  
[gi|12804209|gb|AAH02962.1](#) [Spleen tyrosine kinase \[Homo sapiens\]](#)  
[gi|21361553|ref|NP\\_003168.2](#) [spleen tyrosine kinase \[Homo sapiens\]](#)  
[gi|479013|gb|AAA36526.1](#) [protein tyrosine kinase](#)  
Length=635

Score = 28.6 bits (60), Expect = 30  
Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPHYAPE 13  
 PAQ V+F+PY PE  
 Sbjct 308 PAQGNRQESTVVSFNPVEPE 326

> [gi|448916|prf||1918215A](#) protein Tyr kinase  
 Length=630


Score = 28.6 bits (60), Expect = 30  
 Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPHYAPE 13  
 PAQ V+F+PY PE  
 Sbjct 303 PAQGNRQESTVVSFNPVEPE 321

> [gi|1092813|prf||2101280A](#) p72syk protein  
 Length=365

Score = 28.6 bits (60), Expect = 30  
 Identities = 9/19 (47%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query 2 PAQ-----VAFBPHYAPE 13  
 PAQ V+F+PY PE  
 Sbjct 303 PAQGNRQESTVVSFNPVEPE 321

> [gi|89061682|ref|XP\\_944591.1|](#)  PREDICTED: similar to dynein, axonemal, heavy po-  
 sapiens]  
 Length=4107

Score = 26.1 bits (54), Expect = 174  
 Identities = 9/15 (60%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query 6 AFBP----YAPEPGS 16  
 AF P Y PEPGS  
 Sbjct 3866 AFSPSGLYYTPEPGS 3880

Get selected sequences

Select all

Deselect all

Tree View

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PTR+PRF excludi  
 environmental samples

Posted date: Jun 10, 2006 4:09 AM

Number of letters in database: 1,269,795,892

Number of sequences in database: 3,695,564

Lambda K H  
 0.346 0.288 1.79

Gapped  
 Lambda K H  
 0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 3695564

Number of Hits to DB: 15358398

Number of extensions: 349668

Number of successful extensions: 1740

Number of sequences better than 20000: 1713

Number of HSP's better than 20000 without gapping: 0  
Number of HSP's gapped: 1740  
Number of HSP's successfully gapped: 1740  
Length of query: 18  
Length of database: 1269795892  
Length adjustment: 8  
Effective length of query: 10  
Effective length of database: 1240231380  
Effective search space: 12402313800  
Effective search space used: 12402313800  
T: 11  
A: 40  
X1: 15 (7.5 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 38 (19.3 bits)  
S2: 38 (19.3 bits)